

## SEQUENCE LISTING

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<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
 OF TREATMENT THEREWITH

<130> 08702.0081-00000

<140> 09/249,011

<141> 1999-02-12

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 405

<212> DNA

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(405)

<223> Anti-B7-2 heavy chain

<400> 1

atg	ggt	tgg	aac	tgt	atc	atc	ttc	ttt	ctg	ggt	aca	aca	gct	aca	ggt	48
Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly	
1				5					10					15		

gtg	cac	tcc	cag	gtc	cag	ctg	cag	cag	tct	ggg	cct	gag	ctg	gtg	agg	96
Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Arg	
			20				25						30			

cct	ggg	gaa	tca	gtg	aag	att	tcc	tgc	aag	ggt	tcc	ggc	tac	aca	ttc	144
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				

act	gat	tat	gct	ata	cag	tgg	gtg	aag	cag	agt	cat	gca	aag	agt	cta	192
Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Lys	Gln	Ser	His	Ala	Lys	Ser	Leu	
	50					55					60					

gag	tgg	att	gga	gtt	att	aat	att	tac	tat	gat	aat	aca	aac	tac	aac	240
Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn	
	65				70					75				80		

2

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc 288  
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
                     85                    90                    95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc 336  
 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
                     100                    105                    110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga 384  
 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
                     115                    120                    125

acc tca gtc acc gtc tcc tca 405  
 Thr Ser Val Thr Val Ser Ser  
                     130                    135

<210> 2  
 <211> 135  
 <212> PRT  
 <213> Murine sp.

<220>  
 <223> Anti-B7-2 heavy chain

<400> 2  
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                     1                    5                    10                    15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
                     20                    25                    30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
                     35                    40                    45

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
                     50                    55                    60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
                     65                    70                    75                    80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
                     85                    90                    95

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
                     100                    105                    110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
                     115                    120                    125

Thr Ser Val Thr Val Ser Ser  
                     130                    135

<210> 3  
 <211> 396  
 <212> DNA  
 <213> Murine sp.

3

<220>  
 <221> CDS  
 <222> (1)..(396)  
 <223> Anti-B7-2 light chain

<400> 3

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 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
 1 5 10 15

ggg acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct 96  
 Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
 20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt 144  
 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
 35 40 45

ctg ctg aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag 192  
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg 240  
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80

gaa tct ggg gtc cct gat cgc ttc sca ggc agt gga tct ggg aca gat 288  
 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
 85 90 95

ttc act ctg acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat 336  
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
 100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag 384  
 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
 115 120 125

ctg gaa ata aaa 396  
 Leu Glu Ile Lys  
 130

<210> 4  
 <211> 132  
 <212> PRT  
 <213> Murine sp.

<220>  
 <223> Anti-B7-2 light chain

<400> 4

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
 1 5 10 15

Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala  
 20 25 30

4

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser  
 35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr  
 100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys  
 115 120 125

Leu Glu Ile Lys  
 130

<210> 5  
 <211> 405  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Humanized  
 murine anti-human B7-2 heavy chain

<220>  
 <221> CDS  
 <222> (1)..(405)

<400> 5  
 atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca gct aca ggt 48  
 Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
 1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag 96  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc 144  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc 192  
 Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac 240  
 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
 65 70 75 80

5

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc 288  
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
                     85                    90                    95

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtc 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                     100                    105                    110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt 384  
 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
                     115                    120                    125

acc ctt gtc acc gtc tcc tca 405  
 Thr Leu Val Thr Val Ser Ser  
                     130                    135

&lt;210&gt; 6

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Humanized  
 murine anti-human B7-2 heavy chain

&lt;400&gt; 6

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly  
                     1                    5                    10                    15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                     20                    25                    30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
                     35                    40                    45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
                     50                    55                    60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
                     65                    70                    75                    80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
                     85                    90                    95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                     100                    105                    110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
                     115                    120                    125

Thr Leu Val Thr Val Ser Ser  
                     130                    135

&lt;210&gt; 7

&lt;211&gt; 396

6

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(396)

&lt;400&gt; 7

atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct 48  
 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
 1 5 10 15  
 ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct 96  
 Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
 20 25 30  
 gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt 144  
 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
 35 40 45  
 ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag 192  
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg 240  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat 288  
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat 336  
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110  
 tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag 384  
 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
 115 120 125  
 gtg gaa ata aaa 396  
 Val Glu Ile Lys  
 130

&lt;210&gt; 8

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Humanized  
murine anti-human B7-2 light chain

7

<400> 8  
 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Trp Val Ser  
 1 5 10 15  
 Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
 20 25 30  
 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
 35 40 45  
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110  
 Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
 115 120 125  
 Val Glu Ile Lys  
 130

<210> 9  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR1 of  
 humanized murine anti-human B7-2 heavy chain

<220>  
 <221> CDS  
 <222> (1)..(15)

<400> 9  
 gat tat gct ata cag  
 Asp Tyr Ala Ile Gln  
 1 5

15

<210> 10  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR1 of humanized  
 murine anti-human B7-2 heavy chain

8

<400> 10  
 Asp Tyr Ala Ile Gln  
 1 5

<210> 11  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR2 of  
 humanized murine anti-human B7-2 heavy chain

<220>  
 <221> CDS  
 <222> (1)..(51)

<400> 11  
 gtt att aat att tac tat gat aat aca aac tac aac cag aag ttt aag 48  
 Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
 1 5 10 15

ggc 51  
 Gly

<210> 12  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR2 of humanized  
 murine anti-human B7-2 heavy chain

<400> 12  
 Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
 1 5 10 15

Gly

<210> 13  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR3 of  
 humanized murine anti-human B7-2 heavy chain

<220>  
 <221> CDS  
 <222> (1)..(21)



9

<400> 13  
 gcg gcc tgg tat atg gac tac  
 Ala Ala Trp Tyr Met Asp Tyr  
 1 5

21

<210> 14  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR3 of humanized  
 murine anti-human B7-2 heavy chain

<400> 14  
 Ala Ala Trp Tyr Met Asp Tyr  
 1 5

<210> 15  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR1 of  
 humanized murine anti-human B7-2 light chain

<220>  
 <221> CDS  
 <222> (1)..(51)

<400> 15  
 aaa tcc agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg 48  
 Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
 1 5 10 15

gct 51  
 Ala

<210> 16  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: CDR1 of humanized  
 murine anti-human B7-2 light chain

<400> 16  
 Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu  
 1 5 10 15

Ala

10

<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of  
humanized murine anti-human B7-2 light chain

<220>  
<221> CDS  
<222> (1)..(21)

<400> 17  
tgg gca tcc act agg gaa tct  
Trp Ala Ser Thr Arg Glu Ser  
1 5

21

<210> 18  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR2 of humanized  
murine anti-human B7-2 light chain

<400> 18  
Trp Ala Ser Thr Arg Glu Ser  
1 5

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: CDR3 of  
humanized murine anti-human B7-2 light chain

<220>  
<221> CDS  
<222> (1)..(24)

<400> 19  
acg caa tct tat aat ctt tac acg  
Thr Gln Ser Tyr Asn Leu Tyr Thr  
1 5

24

<210> 20  
<211> 8  
<212> PRT  
<213> Artificial Sequence

11

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: CDR3 of humanized murine anti-human B7-2 light chain

&lt;400&gt; 20

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

&lt;210&gt; 21

&lt;211&gt; 1960

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (12)..(408)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (768)..(1087)

&lt;400&gt; 21

tctagaccac c atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta 50

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu

1

5

10

tgg gta tct ggc acc tgt ggg gac att gtg ctg aca cag tct coa gat 98

Trp Val Ser Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp

15

20

25

tcc ctg gct gta agc tta gga gag agg gcc act att agc tgc aaa tcc 146

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser

30

35

40

45

agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg 194

Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp

50

55

60

tac cag cag aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca 242

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala

65

70

75

tcc act agg gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct 290

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser

80

85

90

ggg aca gat ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg 338

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val

95

100

105

gca gtt tat tac tgc ago caa tct tat aat ctt tac acg ttc gga cag 386

Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln

110

115

120

125

ggg acc aag gtg gaa ata aaa c gtaagtagtc ttctcaactc tagaaattct 438

Gly Thr Lys Val Glu Ile Lys

130

Received from < 617 452 1666 > at 10/11/02 11:00:24 AM [Eastern Daylight Time]

13

tcaaccaaag caaatcttctc aaaagaagaa acctgctata aagagaatca ttcattgcaa 1667  
 catgatataa aataacaaca caataaaagc aattaaataa acanacaata gggaaatggt 1727  
 taagtctatc atggtactta gacttaatgg aatgtcatgc cttatttaca tttttaaaca 1787  
 ggtactgagg gactcctgtc tgccaagggc cgtattgagt actttccaca acctaattta 1847  
 atccacacta tactgtgaga ttaaaaacat tcattaaaat gttgcaaagg ttctataaag 1907  
 ctgagagaca aatatattct ataactcagc aatcccactt ctaggatcaa ttc 1960

<210> 22  
 <211> 239  
 <212> PRT  
 <213> Mus sp.

<400> 22  
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 20 25 30  
 Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
 35 40 45  
 Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80  
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110  
 Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
 115 120 125  
 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
 130 135 140  
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
 145 150 155 160  
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
 165 170 175  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 180 185 190  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 195 200 205

14

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 23  
 <211> 2249  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (12) .. (417)

<220>  
 <221> CDS  
 <222> (655) .. (948)

<220>  
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 <222> (1341) .. (1376)

<220>  
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 <222> (1495) .. (1821)

<220>  
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 <222> (1919) .. (2238)

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 Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr  
 1 5 10

gct aca ggt gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag 98  
 Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu  
 15 20 25

gtg aag aag cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc 146  
 Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  
 30 35 40 45

tac aca ttc act gat tat gct ata cag tgg gtg aga cag gct cct gga 194  
 Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly  
 50 55 60

cag ggc ctc gag tgg att gga gtt att aat att tac tat gat aat aca 242  
 Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr  
 65 70 75

aac tac aac cag aag ttt aag ggc aag gcc aca atg act gta gac aag 290  
 Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys  
 80 85 90

15

tcc acg agc aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat 338  
 Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp  
 95 100 105

acg gcc gtt tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg 386  
 Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp  
 110 115 120 125

ggg caa ggt acc ctt gtc acc gtc tcc tca g gtgagtcctt aaaacctcta 437  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 130 135

gagctttctg gggcgagccg ggcctgactt tggctttggg gcagggagtg ggctaagggtg 497

aggcagggtg cggcagccag gtgcacaccc aatgcccggtg agcccagaca ctggaccctg 557

cctggaccct cgtggataga caagaaccga ggggcctctg cgccctgggc ccagctctgt 617

cccacaccgc ggtcacatgg caaccacctt cttgcag cc tcc acc aag ggc cca 671  
 Ala Ser Thr Lys Gly Pro  
 140

tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca 719  
 Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr  
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gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg 767  
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr  
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gtg tcc tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca 815  
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro  
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gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc 863  
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
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 Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp  
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cac aag ccc agc aac acc aag gtg gac aag aca gtt g gtgagaggcc 958  
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val  
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16

actcccaatc ttctctctgc ag ag cgc aaa tgt tgt gtc gag tgc cca ccg 1369  
 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro  
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tgc cca g gtaagccagc ccaggcctcg ccctccagct caaggcggga caggtgccct 1426  
 Cys Pro  
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 Ala Pro Pro Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro  
 250 255

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc 1583  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 260 265 270 275

gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg 1631  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp  
 280 285 290

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag 1679  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
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 Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val  
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cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac 1775  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 325 330 335

aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa g 1821  
 Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys  
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 Gly Gln Pro Arg Glu Pro  
 355 360

cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag 1983  
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln  
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 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 380 385 390

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc aca 2079  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 395 400 405



17

cct ccc atg ctg gac tcc gac ggc tcc ttc ttc etc tac agc aag etc 2127  
 Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu  
 410 415 420

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc 2175  
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser  
 425 430 435 440

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc etc tcc 2223  
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Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
 115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
 130 135 140

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu  
 145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
 165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
 180 185 190

18

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
 195 200 205  
 Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
 210 215 220  
 Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu  
 225 230 235 240  
 Cys Pro Pro Cys Pro Ala Pro Pro Ala Ala Ala Pro Ser Val Phe Leu  
 245 250 255  
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
 260 265 270  
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln  
 275 280 285  
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys  
 290 295 300  
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu  
 305 310 315 320  
 Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys  
 325 330 335  
 Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys  
 340 345 350  
 Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser  
 355 360 365  
 Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
 370 375 380  
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln  
 385 390 395 400  
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly  
 405 410 415  
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
 420 425 430  
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
 435 440 445  
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 450 455 460